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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=21; hr=9; min=49; sec=55; ms=624;]

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Application No: 10589594

Version No: 3.0

Input Set:

Output Set:

Started: 2008-03-11 13:39:22.927

Finished: 2008-03-11 13:39:23.316

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 389 ms

Total Warnings: 24

Total Errors: 0

No. of SeqIDs Defined: 26

Actual SeqID Count: 26

Error code	Error Description
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Error code

Error Description

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SEQUENCE LISTING

<110> Nakamura, Yusuke
Furukawa, Yoichi

<120> Method for Diagnosing Colorectal Cancers

<130> 082368-008900US

<140> 10589594

<141> 2008-03-11

<150> WO PCT/JP04/02145

<151> 2004-02-24

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2624

<212> DNA

<213> Homo sapiens

<220>

<223> C10orf3

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<221> CDS

<222> (294)...(1688)

<223> C10orf3

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gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcaccgc gctgggcgcc 240
tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
Met
1
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
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cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
20 25 30
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att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
35 40 45
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Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
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aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act				584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr				
85		90	95	
acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg				632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg				
100		105	110	
agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa				680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys				
115		120	125	
caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa				728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys				
130		135	140	145
acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac				776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn				
150		155	160	
tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct				824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala				
165		170	175	
ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc				872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val				
180		185	190	
tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg				920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr				
195		200	205	
gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca				968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser				
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Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu				
230		235	240	
gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag				1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln				
245		250	255	
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Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln				
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aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca				1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala				
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Asp	Val	Gln	His	Leu	Glu	Asp	Asp	Arg	His	Lys	Thr	Glu	Lys	Ile	Gln	
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aag	aag	aga	tcc	gaa	gag	ctc	tta	tct	cag	gtc	cag	ttt	ctt	tac	aca	1304
Lys	Lys	Arg	Ser	Glu	Glu	Leu	Leu	Ser	Gln	Val	Gln	Phe	Leu	Tyr	Thr	
			325					330					335			

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Lys	Ala	Arg	Asn	Gln	Ile	Thr	Gln	Leu	Glu	Ser	Leu	Lys	Gln	Leu	His	
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Glu	Phe	Ala	Ile	Thr	Glu	Pro	Leu	Val	Thr	Phe	Gln	Gly	Glu	Thr	Glu	
			405					410						415		

aac	aga	gaa	aaa	gtt	gcc	gcc	tca	cca	aaa	agt	ccc	act	gct	gca	ctc	1592
Asn	Arg	Glu	Lys	Val	Ala	Ala	Ser	Pro	Lys	Ser	Pro	Thr	Ala	Ala	Leu	
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act	gag	cat	cgc	gat	ctg	ctt	gtc	cat	gtg	gaa	tac	tgt	tca	aag	tag	1688
Thr	Glu	His	Arg	Asp	Leu	Leu	Val	His	Val	Glu	Tyr	Cys	Ser	Lys		
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gctaattgggt	taatgcacca	gcaagcaaaa	tattttatgt	tttggggggt	tgaaaaatca		2048
aagataatta	accaaggatc	ttaactgtgt	tcgcattttt	tatccaagca	cttagaaaac		2108
ctacaatcct	aattttgatg	tccattgtta	agagggtggg	atagatacta	tttttttttt		2168
catattgtat	agcggttatt	agaaaagttg	gggattttct	tgatctttat	tgctgcttac		2228
cattgaaact	taaccagct	gtgttcccca	actctgttct	gcgcacgaaa	cagtatctgt		2288
ttgaggcata	atcttaagt	gccacacaca	atgttttctc	ttatgttatc	tggcagtaac		2348
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gctgggcaat gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt 2528
ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac 2588
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<213> Homo sapiens

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<220>
<223> C10orf3

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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
          35          40          45
Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
 50          55          60
Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
 65          70          75          80
Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
          85          90          95
Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
          100          105          110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
          115          120          125
Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
          130          135          140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
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Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
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Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
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Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
          195          200          205
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          210          215          220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
          225          230          235          240
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          245          250          255
Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
          260          265          270
Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
          275          280          285
Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
          290          295          300
Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
          305          310          315          320
Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
          325          330          335
Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu

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<220>
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<210> 6
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<400> 7
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<210> 8
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<210> 10
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<220>
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<210> 11
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<220>
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<210> 13
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amplification primer

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<210> 18
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<220>
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 DNA fragment insertion site

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 ccatccaggc taacacggtg aaaccccccc ccatctctac taaaaaaaaa aaatacaaaa 180
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